

IN THE SPECIFICATION

Please amend the specification as follows:

Please replace the Sequence Listing of record with the Substitute Sequence Listing submitted herewith.

Please replace the paragraph at page 22, lines 3 to 22 with the following amended paragraph:

Tethers which may be comprised in conjugate peptides of the invention may be identified using the methods set forth in the preceding section. Such tethers may have amino acid compositions which comprise a substantial portion of hydrophobic amino acids such as phenylalanine and tryptophan, and/or a substantial number of serine, threonine, or proline residues. In particular, nonlimiting embodiments, tethers of the invention may comprise amino acid sequences which have the general description hydrophobic - basic - hydrophobic - hydrophobic - hydrophobic (SEQ ID NO:322); Ser/Thr - hydrophobic - hydrophobic - Ser/Thr (SEQ ID NO:323); Ser/Thr - Ser/Thr - hydrophobic - hydrophobic - Ser/Thr - Ser/Thr (SEQ ID NO:324); and Ser/Thr - hydrophobic - hydrophobic - hydrophobic (SEQ ID NO:325). Alternatively, tethers may comprise heat shock binding peptides as described in Blond-Elguindi et al., 1993, Cell 75:717-728, including the consensus sequence hydrophobic - (Trp/X) - hydrophobic - X - hydrophobic -X - hydrophobic (SEQ ID NO:326) and the specific peptides His Trp Asp Phe Ala Trp Pro Trp (SEQ ID NO:143) and Phe Trp Gly Leu Trp Pro Trp Glu (SEQ ID NO:144); Auger et al., 1996, Nature Med. 2:306-310, including Gln Lys Arg Ala Ala (SEQ ID NO:145) and Arg Arg Arg Ala Ala (SEQ ID NO:146); Flynn et al., 1989, Science 245:385-390; Gragerov et al., 1994, J. Mol. Biol. 235:848-854; Terlecky et al., 1992, J. Biol. Chem. 267:9202-9209, Lys Phe Glu Arg Gln (SEQ ID NO:147); and Nieland et al., 1996, Proc. Natl. Acad. Sci. U.S.A. 93:6135-6139, including VsV8 peptide, Arg Gly Tyr Val Tyr Gln Gly Leu (SEQ ID NO:148). In preferred embodiments, tethers of the invention may have a length of 4-50 amino acid residues, and more preferably 7-20 amino acid residues.